



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Weeks, Donald P.
Wang, Xiao-Zhuo
Herman, Patricia L.

(ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND
USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Sheridan Ross P.C.
- (B) STREET: 1700 Lincoln St., Suite 3500
- (C) CITY: Denver
- (D) STATE: Colorado
- (E) COUNTRY: USA
- (F) ZIP: 80203

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/042,666
(B) FILING DATE: 04-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/042,941
(B) FILING DATE: 04-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Crook, Wannell M.
(B) REGISTRATION NUMBER: 31,071
(C) REFERENCE/DOCKET NUMBER: 3553-18

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (303) 863-91
(B) TELEFAX: (303) 863-0223

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

RECEIVED
AUG 20 PAID
GROUP 1800

AUG 25 PAID

GROUP 1800

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or Thr"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Thr	Phe	Val	Arg	Asn	Ala	Trp	Tyr	Val	Ala	Ala	Leu	Pro	Glu	Glu	Leu
1					5				10				15		
Ser	Glu	Lys	Pro	Leu	Gly	Arg	Thr	Ile	Leu	Asp	Xaa	Xaa			
			20					25							

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr	Tyr	Val	Val	Thr	Asp	Ala	Xaa	Ile	Lys	Xaa	Lys	Tyr	Met	Asp	Xaa
1					5				10				15		
Val	Glu	Val	Xaa												
			20												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA	48
Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu	
1 5 10 15	
CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG	96
Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala	
20 25 30	
CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT	144
Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys	
35 40 45	
CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT	192
Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His	
50 55 60	
CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGG CAG TGC	240
Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gln Cys	
65 70 75 80	
GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC	288
Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val	
85 90 95	
CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC	336
Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro	
100 105 110	
GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC	384
Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys	
115 120 125	
CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC	432
Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp	
130 135 140	
TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC	480
Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala	
145 150 155 160	
CAA TAT GTC CAT CGC GCC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG	528

Gln	Tyr	Val	His	Arg	Ala	Asn	Ala	Gln	Thr	Asp	Ala	Phe	Asp	Arg	Leu	
165								170						175		
GAG	CGC	GAG	GTG	ATC	GTC	GGC	GAC	GGT	GAG	ATA	CAG	GCG	CTG	ATG	AAG	576
Glu	Arg	Glu	Val	Ile	Val	Gly	Asp	Gly	Glu	Ile	Gln	Ala	Leu	Met	Lys	
180							185						190			
ATT	CCC	GGC	GGC	ACG	CCG	AGC	GTG	CTG	ATG	GCC	AAG	TTC	CTG	CGC	GGC	624
Ile	Pro	Gly	Gly	Thr	Pro	Ser	Val	Leu	Met	Ala	Lys	Phe	Leu	Arg	Gly	
195							200						205			
GCC	AAT	ACC	CCC	GTC	GAC	GCT	TGG	AAC	GAC	ATC	CGC	TGG	AAC	AAG	GTG	672
Ala	Asn	Thr	Pro	Val	Asp	Ala	Trp	Asn	Asp	Ile	Arg	Trp	Asn	Lys	Val	
210							215						220			
AGC	GCG	ATG	CTC	AAC	TTC	ATC	GCG	GTG	GCG	CCG	GAA	GGC	ACC	CCG	AAG	720
Ser	Ala	Met	Leu	Asn	Phe	Ile	Ala	Val	Ala	Pro	Glu	Gly	Thr	Pro	Lys	
225							230				235			240		
GAG	CAG	AGC	ATC	CAC	TCG	CGC	GGT	ACC	CAT	ATC	CTG	ACC	CCC	GAG	ACG	768
Glu	Gln	Ser	Ile	His	Ser	Arg	Gly	Thr	His	Ile	Leu	Thr	Pro	Glu	Thr	
245							250						255			
GAG	GCG	AGC	TGC	CAT	TAT	TTC	TTC	GGC	TCC	TCG	CGC	AAT	TTC	GGC	ATC	816
Glu	Ala	Ser	Cys	His	Tyr	Phe	Phe	Gly	Ser	Ser	Arg	Asn	Phe	Gly	Ile	
260							265						270			
GAC	GAT	CCG	GAG	ATG	GAC	GGC	GTG	CTG	CGC	AGC	TGG	CAG	GCT	CAG	GCG	864
Asp	Asp	Pro	Glu	Met	Asp	Gly	Val	Leu	Arg	Ser	Trp	Gln	Ala	Gln	Ala	
275							280						285			
CTG	GTC	AAG	GAG	GAC	AAG	GTC	GTC	GAG	GCG	ATC	GAG	CGC	CGC	CGC	CGC	912
Leu	Val	Lys	Glu	Asp	Lys	Val	Val	Val	Glu	Ala	Ile	Glu	Arg	Arg	Arg	
290							295						300			
GCC	TAT	GTC	GAG	GCG	AAT	GGC	ATC	CGC	CCG	GCG	ATG	CTG	TCG	TGC	GAC	960
Ala	Tyr	Val	Glu	Ala	Asn	Gly	Ile	Arg	Pro	Ala	Met	Leu	Ser	Cys	Asp	
305							310						315			
GAA	GCC	GCA	GTC	CGT	GTC	AGC	CGC	GAG	ATC	GAG	AAG	CTT	GAG	CAG	CTC	1008
Glu	Ala	Ala	Val	Arg	Val	Ser	Arg	Glu	Ile	Glu	Lys	Leu	Glu	Gln	Leu	
325							330						335			
GAA	GCC	GCC	TGA													1020
Glu	Ala	Ala	*													
340																

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
1 5 10 15

Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
20 25 30

Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
35 40 45

Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
50 55 60

Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gln Cys
65 70 75 80

Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
85 90 95

Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro
100 105 110

Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys
115 120 125

Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp
130 135 140

Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala
145 150 155 160

Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu
165 170 175

Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys
180 185 190

Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly
195 200 205

Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val
210 215 220

Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys
225 230 235 240

Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr
245 250 255

Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile
260 265 270

Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
275 280 285

Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
290 295 300

Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
305 310 315 320

Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
325 330 335

Glu Ala Ala *
340

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG ACC TAT GTC GTC ACC GAC GCC TGC ATC AAG TGC AAG TAC ATG GAC	48
Met Thr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp	
1 5 10 15	
TGC GTG GAA GTC TGC CCT GTG GAC TGC TTC TAC GAA GGC GAG AAC ATG	96
Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met	
20 25 30	
CTC GTC ATC AAT CCC AGT GAA TGC ATC GAC TGC GGC GTC TGC GAA CCG	144
Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro	
35 40 45	
GAA TGC CCA GCC GAA GCC ATC CTT CCC GAC ACC GAA AGC GGT CTC GAG	192
Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu	
50 55 60	
CAG TGG ATG GAA CTG AAC ACG AAG TAC TCG GCC GAG TGG CCG AAT CTC	240
Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu	
65 70 75 80	
ACG TCC AAG AAA GAT TCG CCG GAA GAT GCC GAC GAG TAC AAG GGC GTG	288
Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val	
85 90 95	
GAA GGC AAG TTC GAG AAG TTC TCG CCC GAG CCC GGC GAG GGC GAC	336
Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp	
100 105 110	
TGA	339
*	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Thr	Tyr	Val	Val	Thr	Asp	Ala	Cys	Ile	Lys	Cys	Lys	Tyr	Met	Asp
1				5					10					15	
Cys	Val	Glu	Val	Cys	Pro	Val	Asp	Cys	Phe	Tyr	Glu	Gly	Glu	Asn	Met
		20						25					30		
Leu	Val	Ile	Asn	Pro	Ser	Glu	Cys	Ile	Asp	Cys	Gly	Val	Cys	Glu	Pro
		35				40						45			
Glu	Cys	Pro	Ala	Glu	Ala	Ile	Leu	Pro	Asp	Thr	Glu	Ser	Gly	Leu	Glu
	50				55					60					
Gln	Trp	Met	Glu	Leu	Asn	Thr	Lys	Tyr	Ser	Ala	Glu	Trp	Pro	Asn	Leu
	65				70				75			80			
Thr	Ser	Lys	Lys	Asp	Ser	Pro	Glu	Asp	Ala	Asp	Glu	Tyr	Lys	Gly	Val
		85					90					95			
Glu	Gly	Lys	Phe	Glu	Lys	Phe	Phe	Ser	Pro	Glu	Pro	Gly	Glu	Gly	Asp
	100						105					110			

*